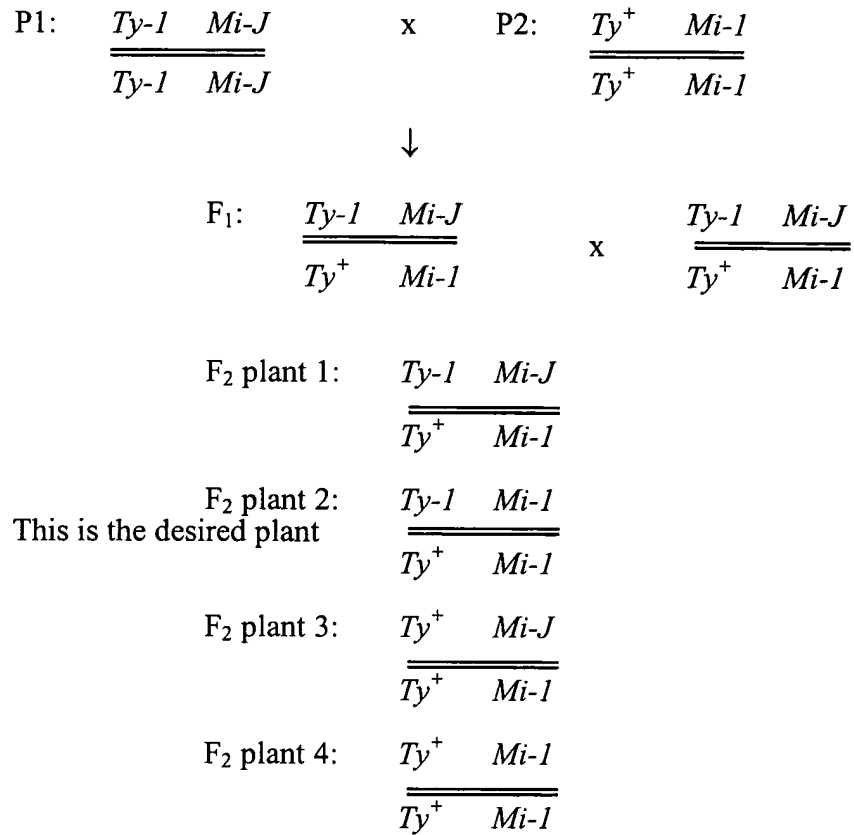


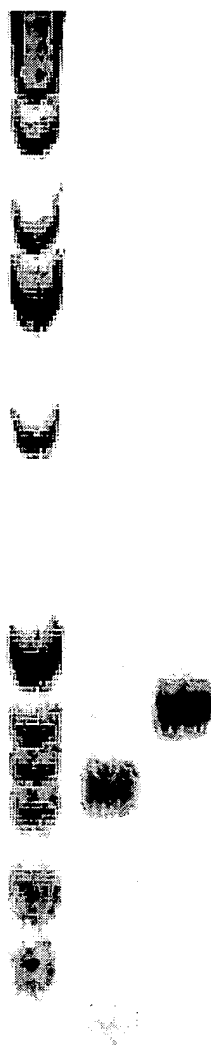
FIGURE 1



as well as other genotypes would be produced in the F2. By selfing plant number 2 completely homozygous plants for *Ty-l* and *Mi-l* can be identified.

FIGURE 2

A B



Ty-1 assay

A = resistant allele, 303 & 95
bp

B = susceptible allele, 398 bp

FIGURE 3



FIGURE 4

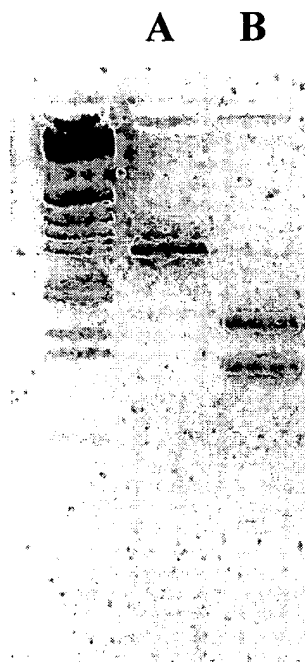


FIGURE 5

Ty-/- SEQ ID NO.: 10

Ty+/- SEQ ID NO.: 11

SEQ ID NO:1

5' T A A T C C G T C G T T A C C T C T C C T T

1 C T A A T C C G T C G T T A C C T C T C C T T T G A A C T A A A A T T T T T T T G T C A A A A G T Ty-/-
1 C T A A T C C G T C G T T A C C T C T C C T T T G A A C T A A A A T T T T T T T G T C A A A A G T Ty+/-

51 A C A A A T C T G T T T A T T T T A T A T T T T T T T T T T G G A A T T T A C T A T C G A T T A Ty-/-
51 A C A A A T C T G T T T A T T T T A T A T T T T T T T T T T G G A A T T T A C T A T C T T T A Ty+/-

101 T T T T G T A A T T A G A A G G T T A G A A T T G G A G T A T A T G T T G T G A T T G G A A C Ty-/-
100 T T T T G T A A T T A G A A G G T T A G A A T T G G A G T A T A T G T T G T G A T T G G A A C Ty+/-

151 A T T T G T T G T T G C C T T T A T G G T G G C A A T T A T G T T T A C A T G T G T C A T T G G C Ty-/-
150 A T T T G T T T T G C C T T T A T G G T G G C A A T T A T G T T T A C A T G T G T C A T T G G C Ty+/-

201 A A C T T A C T G A G T C A T C T T T A C T T T T T A A T A A G A A T G C T T T C A A A T G T T T A Ty-/-
200 A A C T T A C T G A G T C A T C T T T T T T A A T A A G A A T G C T T T C A A A T G T T T A Ty+/-

251 A A T T T C A T T A G C T C A A T G G T A A T T G T A T T T A T T G A T G C A T A T A T C T T T T Ty-/-
250 A A T T C A T T A G C T C A A T G G T A A T T G T A T T T A T T G A T G C A T A T A T C T T T T Ty+/-

301 T G T T C T A G T T T C T G A T T A T A T C A T G T A N C G A A A C T T A T A T A A A A A T A A Ty-/-
300 T G T T C T A G T T T C T G A T T A T A T C A T G T A C G A A A C T T A T A T A A A A A A T A A Ty+/-

351 T A G T A A T A G T A G T A G A A N A T T T A T G A C A T C A T T G C T A T T G A A G T C A T C C Ty-/-
350 T A G T A A T A G T A G T A G A A N A T T T A T G A C A T C A T T G C T A T T G A A G T C A T C C Ty+/-

AGT AACGATAACTTCAGTAGGC

401 G A A T C T

399 G A A T C T A M C

SEQ ID NO:2

FIGURE 6

Mi+ - SEQ ID NO.: 7
 Mi-1 - SEQ ID NO.: 8
 Mi-J - SEQ ID NO.: 9

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1  GACACGGACCCACTATTCTGAAACTGATGGTCATTCTTTCTCTCCCTATCGGAGCCTTGCTGATTTCCACTCTTGCAGCACAATGACTAGCTTGAC  Mi+.seq
1  GACACGGACCCACTATTCTGAAAGCAGATGGTCATTCTTTCTCTCCCTATCGGAGCCTTGCTGATTTCCGCTCTTGCAGCACAATGACTAGCTTGAC  Mi-1.seq
1  GACACGGACCCACTATTCTGAAACTGATGGTCATTCTTTCTCTCCCTATCGGAGCCTTGCTGATTTCCACTCTTGCAGCACAATGACTAGCTTGAC  Mi-J.seq

101 GTAAAGGGATCTGCACCTTACATCGGTATCCTGTTGAGTTGCATAACCCAGAAACCTTGGACTTTGCTTTGACTTTTTTACCTGATTCACGATGACACCTTT  Mi+.seq
101 GTAAAGGGATCTGCACCTTACATCGGTATCCTGTTGAGTTGCATAACCCAGAAACCTTGGACTTTGCTTTGACTTTTTTACCTGATTCACGATGACACCTTT  Mi-1.seq
101 GTAAAGGGATCTGCACCTTACATCGGTATCCTGTTGAGTTGCATAACCCAGAAACCTTGGACTTTGCTTTGACTTTTTTACCTGATTCACGATGACACCTTT  Mi-J.seq

201 CTCCTCTAATTCAGCTTCAGATATAGATCATAACTCTTGCCATTGCAGGCATTATCCCTCTTAACCATACTGGATTATTGGAGAACCCATCATTTTCA  Mi+.seq
201 CTCCTCTAATTCAGCTTCAGATATAGATCATAACTCTTGCCATTGCAGGCATTATCCCTCTTAACCATACTGGATTATTGGAGAACCCATCATTTTCA  Mi-1.seq
201 CTCCTCTAATTCAGCTTCAGATATAGATCATAACTCTTGCCATTGCAGGCATTATCCCTCTTAACCATACTGGATTATTGGAGAACCCATCATTTTCA  Mi-J.seq

301 CCATCAGAAGACCTCTTTGGGACTACAAGTGGGTAAAGCTGAAGAGGGAGCAACAGAGGTCGCGAATTGCATAGATCCCTTTGTGAAGAAATCTGCAGCTT  Mi+.seq
301 CCATCAGAAGACCTCTTTGGGACTACAAGTGGGTAAAGCTGAAGAGGGAGCAACAGAGGTCGCGAATTGCATAGATCCCTTTGTGAAGAAATCTGCAGCTT  Mi-1.seq
301 CCATCAGAAGACCTCTTTGGGACTACAAGTGGGTAAAGCTGAAGAGGGAGCAACAGAGGTCGCGAATTGCATAGATCCCTTTGTGAAGAAATCTGCAGCTT  Mi-J.seq

401 TABCACTCAACAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTCTCTTTTAACTTGACCTGTTCCAGCACTACCTTTGCTTGCACTAGTGTG  Mi+.seq
401 TABCACTCAACAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTCTCTTTTAACTTGACCTGTTCCAGCACTACCTTTGCTTGCACTAGTGTG  Mi-1.seq
401 TABCACTCAACAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTCTCTTTTAACTTGACCTGTTCCAGCACTACCTTTGCTTGCACTAGTGTG  Mi-J.seq

501 CTTCCGGTCAGACAAGGAGACCCCTTGCTACCTTTTCTCTTCCCTGGAGATGTCAATACATATTTTCCATAGAAATCTGGGATACATGTCAAGGAATCT  Mi+.seq
501 CTTCCGGTCAGACAAGGAGACCCCTTGCTACCTTTTCTCTTCCCTGGAGATGTCAATACATATTTTCCATAGAAATCTGGGATACATGTCAAGGAATCT  Mi-1.seq
501 CTTCCGGTCAGACAAGGAGACCCCTTGCTACCTTTTCTCTTCCCTGGAGATGTCAATACATATTTTCCATAGAAATCTGGGATACATGTCAAGGAATCT  Mi-J.seq

601 CCGAGTTCTCTCCCTTTCTCTTAATCGGAGAAATCATTATTGTACACTTCCCTTATGCCCTGACACATCGGAATATAGCTTCTGGGTTCTTTGCTG  Mi+.seq
601 CCGAGTTCTCTCCCTTTCTCTTAATCGGAGAAATCATTATTGTACACTTCCCTTATGCCCTGACACATCGGAATATAGCTTCTGGGTTCTTTGCTG  Mi-1.seq
601 CCGAGTTCTCTCCCTTTCTCTTAATCGGAGAAATCATTATTGTACACTTCCCTTATGCCCTGACACATCGGAATATAGCTTCTGGGTTCTTTGCTG  Mi-J.seq

701 AAACCAAGTCCTTCTTTGAATCATCCTCTGAGTCCCTGTTCTTACATTGTCAGGAATCATCTCTGGCATTTTACTGCTTGAACCTCCATCTAGACTTTTC  Mi+.seq
701 AAACCAAGTCCTTCTTTGAATCATCCTCTGAGTCCCTGTTCTTACATTGTCAGGAATCATCTCTGGCATTTTACTGCTTGAACCTCCATCTAGACTTTTC  Mi-1.seq
701 AAACCAAGTCCTTCTTTGAATCATCCTCTGAGTCCCTGTTCTTACATTGTCAGGAATCATCTCTGGCATTTTACTGCTTGAACCTCCATCTAGACTTTTC  Mi-J.seq

801 AACCAACAGGGCCCAAGGCTCTGGTTCTGTCATCGAGTGCATCATCTTGTATAAATTTTTTGGAGATACATCTGATCCACCTCATTGTTCTTCTCTA  Mi+.seq
801 AACCAACAGGGCCCAAGGCTCTGGTTCTGTCATCGAGTGCATCATCTTGTATAAATTTTTTGGAGATACATCTGATCCACCTCATTGTTCTTCTCTA  Mi-1.seq
801 AACCAACAGGGCCCAAGGCTCTGGTTCTGTCATCGAGTGCATCATCTTGTATAAATTTTTTGGAGATACATCTGATCCACCTCATTGTTCTTCTCTA  Mi-J.seq

901 TTTCATCTCTCCCTAG
901 TTTCATCTCTCCCTAG
901 TTTCATCTCTCCCTAG
  
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Decoration 'Decoration #1': Shade (with solid deep red) residues that differ from Mi+.seq.
 Decoration 'Decoration #2': Shade (with solid bright cobalt) residues that differ from Mi-J.seq.

FIGURE 7

Mi+ (SEQ ID. NO. 7)

GACACGGACCCACTATTCTGAAACTGATGGTCATTCTTTCTCTCCTTATCGGAGCCTTGGTCTGAGTTTCCAGTCTTGCA
AGCAAAGTGACTAGCTTGACGTAAGGGATCTGCACCTACATCGGTATCCTGTTGAGTTGCATAACCAGAAACCATGGACT
TTGCTTTGACTTTTTTACCTGATTACGATGAACATCTTTCTCCTCTAATTCAGCTTCAGATAAATAGATCATAACTCTTG
CCATTGCAGGCATTATCCTTCTTAACCATACTGGATTATTGGAGAACACATCATTTTACCATCAGAAGACCTCTTGGG
ACTAGAAGTGGGTAAGGCTGAAGAGGGAGCAACAGAAGGTCGCGAATTGCATAGATCCTTTTGTGAAGAATCTGCAGCTT
TAACACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTGTTCCCTTTTAACTTGACCTGTTCCAGCACTA
CCTTTGCTTGCACCTAGTGTCTTCCGGTCAGACAAGGAGACCCTTGCTACCTTTTCCCTTCTAGAGATGTCATCACATAT
TTTTTCCATAGAATCCTGGGATTACATGTCAAGGAATCTCGCAGTTCTCTCCCTTTTCTCTTAATCGGAGAATCATTAT
TGTCACACTTCCCTTATGCGTTGACACATCGGAAATATAAGCTTCTGGGTTCTTTGCTGAAACCAAGTCTTTCTTTGAA
TCATCCTCTGAGTCCCTGTTCTTACATTTGTACGAATCATCTCTGGCATTCTTACTGCTTGAACCTCCATCTAGACTTTTC
AACAAACAGGGCAAAAGGTCCTGTTCTCGTCATCGAGTGCAATCTTGTATAATTTTTTGGGAAGATACATCTGATTCCA
CTTCACTTGTGTTCCCTTCTATTGTCATCCTCCGTAG

Mi-1 (SEQ ID. NO. 8)

GACACGGACCCACTATTCTGAAACCGATGGTCATTCTTTCTCTCCTTATCGGAGCCTTGGTCTGAATTTCCCGTCTTGCA
AGCAAATTGACTAGCTTGACGTAAGGGATCTGCACCTGCATCGGTATCCTGTTGAGTTGCATAACCAGAAACCGTGGACT
TTGCTTTGACTTTTTTACCTGATTACGATGGACATCTTTCTCCTCTAATTCAGCTTCAGATAAATAGATCATAACTCTTG
CCATTGCAGGCATTATCCTTCTTAACCATACTGGATTATTGGAGAACCACATCATTTTACCATCAGAAGACCTCTTGGC
ACTAGAAGTGGGAAAGGCTGAAGAGGGAGCAACAGAAGGTCGCGAATTGCATAGATCCTTTTGTGAAGAATCTGCAGCTT
TAACACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTGTTCCCTTTTAACTTGACCTGTTCCAGCACTA
CCTTTGCTTGCACCTAGTGTCTTCCGGTCAGACAAGGAGACCCTTGCTACCTTTTCCCTTCTGGAGATGTCATCACATAT
TTTTTCCATAGAATCTTGGGATTACATGTCAAGGAATCTCGAAGTTCTCTCCCTTTTCTCTTAATCGGAGAATCATTAT
TGTCACACTTCCCTTATGCGTTGACACATCGGAAATATAAGCTTCTGGGTTCTTTGCTGAAACCAAGTCTTTCTTTGAA
TCATCCTCTGAGTCCCTGTTCTTACATTTCTCACGAATCATCTCTGGCATTCTTACTGCTTGAACCTCCATCTAGACTTTTC
AACAAACAGGGCAGAAGGTCCTGTTCTCGTCATCGAGTGCAATCTTGTATAATTTTTTGGGAAGATACATCTGATTCCA
CCTCACTTGTGTTCCCTTCTATTGTCATCCTCCGTAG

Mi-J (SEQ ID. NO. 9)

GACACGGACCCACTATTCTGAAACTGATGGTCATTCTTTCTCTCCTTATCGGAGCCTTGGTCTGACTTTCCAGTCTTGCA
AGCAAATTGACTAGCTTGACGTAAGGGATCTGCACCTACATCGGTATCCTGTTGAGTTGCATAACCAGAAACCGTGGACT
TTGCTTTGACTTTTTTACCTGATTACGATGGACAACCTTTCTCCTCTAATTCAGCTTCAGATAAATAGATCATAACTCTTG
CCATTGCAGGCATTATCCTTCTTAACCATACTGGATTATTGGAGAACCACATCATTTTACCATCAGAAGACCTCTTGGG
ACTAGAAGTGGGTAAGGCTGAAGAGGGAGCAACAGAAGGTCGCGAATTGCATAGATCCTTTTGTGAAGAATCTGCAGCTT
TAACACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTGTTCCCTTTTAACTTGACCTGTTCCAGCACTA
CCTTTGCTTGCACCTAGTGTCTTCCGGTCAGACAAGGAGACCCTTGCTACCTTTTCCCTTCTGGAGATGTCATCACATAT
TTTTTCCATAGAATCTTGGGATTACATGTCAAGGAATCTCGAAGTTCTCTCCCTTTTCTCTTAATCGGAGAATCATTAT
TGTCACACTTCCCTTATGCGTTGACACATCGGAAATATAAGCTTCTGGGTTCTTTGCTGAAACCAAGTCTTTCTTTGAA
TCATCCTCTGAGTCCCTGTTCTTACATTTGTATGAATCATCTCTGGCATTCTTACTGCTTGAACCTCCATCTAGACTTTTC
AACAAACAGGGCAGAAGGTCCTGTTCTCGTCATCGAGTGCAATCTTGTATAATTTTTTGGGAAGATACATCTGATTCCA
CCTCACTTGTGTTCCCTTCTATTGTCATCCTCCGTAG

Ty-1 (SEQ ID. NO. 10)

CTAATCCGTCGTTACCTCTCCTTTGAACTAAAAATTTTTTGTCAAAGTTACAAATCTGTTTATTTTATATATTTTTTTT
CTTGGAATTACTATCGATATTTTTGTAATTAGAAGGTTAGAATTGGAGTATATATGTTGTGATTGGAACGATTGTTGTT
GCCTTTATGGTGGCAATTATGTTTACATGTGTCAATGGCTAACTTACTGAGTCATCTTACTTTTTTAATAAGAATGCTTC
AAATGTTTATAATTTCACTAGCTCAATGGTAATTGTATTTATTGATGCATATATCTTTTTTGTCTAGTTTCTGATTATA
TCATGTANCGAACTTATATAAAAAATAATTAGTAATAGTAGTAGAANATTTATGACATCATTGCTATTGAAGTCATCCG
GAATCT

Ty + (SEQ ID. NO. 11)

CTAATCCGTCGTTACCTCTCCTTTGAACTAAAAATTTGTTGTCAAAGTTACAAATCTGTTTATTTTATATACTTTTTTC
TTGGAATTACTATCTTTATTTTTGTAATTAGAAGGTTAGAATTGGAGTATATATGTTGTGATTGGAACGAGTTGCTATTG
CCTTTATGGTGGAAATTATGTTTACATGTGTCAATGGGTAACCTTACTGAGTCATCTTACTTTTTTAATAAGAATGCTTCA
TATGTTTATAATTTCACTAGCTCAATGGTTATTGTATTTATTGATGCATATATCTTTTTTGTCTAGTTTCTGATTATAT
CATGTAGCGAACTTATATAAAAAATAATTAGTAATAGTAGTAGAATTTATGACATCATTGCTATTGAAGTCATCCGGA
ATCTANCT

Figure 8 - Normalized Pathology Scoring

